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RAW SEQUENCE LISTING

DATE: 05/07/2002

PATENT APPLICATION: US/09/778,187B

TIME: 13:59:49

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF3\05072002\I778187B.raw

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3 <110> APPLICANT: Baum, Peter R.
4     Fanslow III, William C
6 <120> TITLE OF INVENTION: MOLECULES DESIGNATED LDCAM
8 <130> FILE REFERENCE: 2873-US
10 <140> CURRENT APPLICATION NUMBER: US 09/778,187B
11 <141> CURRENT FILING DATE: 2001-02-06
13 <150> PRIOR APPLICATION NUMBER: PCT/US99/17905
14 <151> PRIOR FILING DATE: 1999-08-05
16 <150> PRIOR APPLICATION NUMBER: US 60/095,672
17 <151> PRIOR FILING DATE: 1998-08-07
19 <160> NUMBER OF SEQ ID NOS: 10
21 <170> SOFTWARE: PatentIn version 3.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1598
25 <212> TYPE: DNA
26 <213> ORGANISM: homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (16)..(1341)
31 <223> OTHER INFORMATION:
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35           Met Ala Ser Val Val Leu Pro Ser Gly Ser Gln Cys
36           1             5             10
38 gcg gcg gca gcg gcg gcg gcg cct ccc ggg ctg cgg ctg cgg ctt      99
39 Ala Ala Ala Ala Ala Ala Ala Pro Pro Gly Leu Arg Leu Arg Leu
40           15             20             25
42 ctg ctg ttg ctg ttc tcc gcc gcg gca ctg atc ccc aca ggt gat ggg      147
43 Leu Leu Leu Leu Phe Ser Ala Ala Ala Leu Ile Pro Thr Gly Asp Gly
44           30             35             40
46 cag aat ctg ttt acg aaa gac gtg aca gtg atc gag gga gag gtt gcg      195
47 Gln Asn Leu Phe Thr Lys Asp Val Thr Val Ile Glu Gly Glu Val Ala
48 45           50             55             60
50 acc atc agt tgc caa gtc aat aag agt gac gac tct gtg att cag cta      243
51 Thr Ile Ser Cys Gln Val Asn Lys Ser Asp Asp Ser Val Ile Gln Leu
52           65             70             75
54 ctg aat ccc aac agg cag acc att tat ttc agg gac ttc agg cct ttg      291
55 Leu Asn Pro Asn Arg Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu
56           80             85             90
58 aag gac agc agg ttt cag ttg ctg aat ttt tct agc agt gaa ctg aaa      339
59 Lys Asp Ser Arg Phe Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys
60           95             100            105
62 gta tca ttg aca aac gtc tca att tct gat gaa gga aga tac ttt tgc      387

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63 Val Ser Leu Thr Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys
64      110                      115                      120
66 cag ctc tat acc gat ccc cca cag gaa agt tac acc acc atc aca gtc      435
67 Gln Leu Tyr Thr Asp Pro Pro Gln Glu Ser Tyr Thr Thr Ile Thr Val
68 125                      130                      135                      140
70 ctg gtc cca cca cgt aat ctg atg atc gat atc cag aaa gac act gcg      483
71 Leu Val Pro Pro Arg Asn Leu Met Ile Asp Ile Gln Lys Asp Thr Ala
72                      145                      150                      155
74 gtg gaa ggt gag gag att gaa gtc aac tgc act gct atg gcc agc aag      531
75 Val Glu Gly Glu Glu Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys
76                      160                      165                      170
78 cca gcc acg act atc agg tgg ttc aaa ggg aac aca gag cta aaa ggc      579
79 Pro Ala Thr Thr Ile Arg Trp Phe Lys Gly Asn Thr Glu Leu Lys Gly
80                      175                      180                      185
82 aaa tcg gag gtg gaa gag tgg tca gac atg tac act gtg acc agt cag      627
83 Lys Ser Glu Val Glu Glu Trp Ser Asp Met Tyr Thr Val Thr Ser Gln
84 190                      195                      200
86 ctg atg ctg aag gtg cac aag gag gac gat ggg gtc cca gtg atc tgc      675
87 Leu Met Leu Lys Val His Lys Glu Asp Asp Gly Val Pro Val Ile Cys
88 205                      210                      215                      220
90 cag gtg gag cac cct gcg gtc act gga aac ctg cag acc cag cgg tat      723
91 Gln Val Glu His Pro Ala Val Thr Gly Asn Leu Gln Thr Gln Arg Tyr
92                      225                      230                      235
94 cta gaa gta cag tat aag cct caa gtg cac att cag atg act tat cct      771
95 Leu Glu Val Gln Tyr Lys Pro Gln Val His Ile Gln Met Thr Tyr Pro
96                      240                      245                      250
98 cta caa ggc tta acc cgg gaa ggg gac gcg ctt gag tta aca tgt gaa      819
99 Leu Gln Gly Leu Thr Arg Glu Gly Asp Ala Leu Glu Leu Thr Cys Glu
100                      255                      260                      265
102 gcc atc ggg aag ccc cag cct gtg atg gta act tgg gtg aga gtc gat      867
103 Ala Ile Gly Lys Pro Gln Pro Val Met Val Thr Trp Val Arg Val Asp
104 270                      275                      280
106 gat gaa atg cct caa cac gcc gta ctg tct ggg ccc aac ctg ttc atc      915
107 Asp Glu Met Pro Gln His Ala Val Leu Ser Gly Pro Asn Leu Phe Ile
108 285                      290                      295                      300
110 aat aac cta aac aaa aca gat aat ggt aca tac cgc tgt gaa gct tca      963
111 Asn Asn Leu Asn Lys Thr Asp Asn Gly Thr Tyr Arg Cys Glu Ala Ser
112                      305                      310                      315
114 aac ata gtg ggg aaa gct cac tcg gat tat atg ctg tat gta tac gat      1011
115 Asn Ile Val Gly Lys Ala His Ser Asp Tyr Met Leu Tyr Val Tyr Asp
116                      320                      325                      330
118 ccc ccc aca act atc cct cct ccc aca aca acc acc acc acc acc acc      1059
119 Pro Pro Thr Thr Ile Pro Pro Pro Thr Thr Thr Thr Thr Thr Thr Thr
120                      335                      340                      345
122 acc acc acc acc acc atc ctt acc atc atc aca gat tcc cga gca ggt      1107
123 Thr Thr Thr Thr Thr Ile Leu Thr Ile Ile Thr Asp Ser Arg Ala Gly
124 350                      355                      360
126 gaa gaa ggc tcg atc agg gca gtg gat cat gcc gtg atc ggt ggc gtc      1155
127 Glu Glu Gly Ser Ile Arg Ala Val Asp His Ala Val Ile Gly Gly Val

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128 365          370          375          380
130 gtg gcg gtg gtg gtg ttc gcc atg ctg tgc ttg ctc atc att ctg ggg      1203
131 Val Ala Val Val Val Phe Ala Met Leu Cys Leu Leu Ile Ile Leu Gly
132          385          390          395
134 cgc tat ttt gcc aga cat aaa ggt aca tac ttc act cat gaa gcc aaa      1251
135 Arg Tyr Phe Ala Arg His Lys Gly Thr Tyr Phe Thr His Glu Ala Lys
136          400          405          410
138 gga gcc gat gac gca gca gac gca gac aca gct ata atc aat gca gaa      1299
139 Gly Ala Asp Asp Ala Ala Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu
140          415          420          425
142 gga gga cag aac aac tcc gaa gaa aag aaa gag tac ttc atc      1341
143 Gly Gly Gln Asn Asn Ser Glu Glu Lys Lys Glu Tyr Phe Ile
144          430          435          440
146 tagatcagcc tttttgtttc aatgaggtgt ccaactggcc ctatttagat gataaagaga      1401
148 cagtgatatt ggaacttgcg agaaattcgt gtgttttttt atgaatgggt ggaaaggtgt      1461
150 gagactggga aggcttgga tttgctgtgt aaaaaaaaaa aaaaaatgtt ctttggaag      1521
152 aaaaaagcgg ccgctttctt attctatttc aacattcagc ttaatcataa tcctaaaatc      1581
154 atacatgcta tttccat      1598
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158 <211> LENGTH: 442
159 <212> TYPE: PRT
160 <213> ORGANISM: homo sapiens
162 <400> SEQUENCE: 2
164 Met Ala Ser Val Val Leu Pro Ser Gly Ser Gln Cys Ala Ala Ala Ala
165 1          5          10          15
167 Ala Ala Ala Ala Pro Pro Gly Leu Arg Leu Arg Leu Leu Leu Leu Leu
168          20          25          30
170 Phe Ser Ala Ala Ala Leu Ile Pro Thr Gly Asp Gly Gln Asn Leu Phe
171          35          40          45
173 Thr Lys Asp Val Thr Val Ile Glu Gly Glu Val Ala Thr Ile Ser Cys
174          50          55          60
176 Gln Val Asn Lys Ser Asp Asp Ser Val Ile Gln Leu Leu Asn Pro Asn
177 65          70          75          80
179 Arg Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu Lys Asp Ser Arg
180          85          90          95
182 Phe Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys Val Ser Leu Thr
183          100          105          110
185 Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys Gln Leu Tyr Thr
186          115          120          125
188 Asp Pro Pro Gln Glu Ser Tyr Thr Thr Ile Thr Val Leu Val Pro Pro
189          130          135          140
191 Arg Asn Leu Met Ile Asp Ile Gln Lys Asp Thr Ala Val Glu Gly Glu
192 145          150          155          160
194 Glu Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr
195          165          170          175
197 Ile Arg Trp Phe Lys Gly Asn Thr Glu Leu Lys Gly Lys Ser Glu Val
198          180          185          190
200 Glu Glu Trp Ser Asp Met Tyr Thr Val Thr Ser Gln Leu Met Leu Lys
201          195          200          205

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203 Val His Lys Glu Asp Asp Gly Val Pro Val Ile Cys Gln Val Glu His
204      210      215      220
206 Pro Ala Val Thr Gly Asn Leu Gln Thr Gln Arg Tyr Leu Glu Val Gln
207 225      230      235      240
209 Tyr Lys Pro Gln Val His Ile Gln Met Thr Tyr Pro Leu Gln Gly Leu
210      245      250      255
212 Thr Arg Glu Gly Asp Ala Leu Glu Leu Thr Cys Glu Ala Ile Gly Lys
213      260      265      270
215 Pro Gln Pro Val Met Val Thr Trp Val Arg Val Asp Asp Glu Met Pro
216      275      280      285
218 Gln His Ala Val Leu Ser Gly Pro Asn Leu Phe Ile Asn Asn Leu Asn
219      290      295      300
221 Lys Thr Asp Asn Gly Thr Tyr Arg Cys Glu Ala Ser Asn Ile Val Gly
222 305      310      315      320
224 Lys Ala His Ser Asp Tyr Met Leu Tyr Val Tyr Asp Pro Pro Thr Thr
225      325      330      335
227 Ile Pro Pro Pro Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr
228      340      345      350
230 Thr Ile Leu Thr Ile Ile Thr Asp Ser Arg Ala Gly Glu Glu Gly Ser
231      355      360      365
233 Ile Arg Ala Val Asp His Ala Val Ile Gly Gly Val Val Ala Val Val
234      370      375      380
236 Val Phe Ala Met Leu Cys Leu Leu Ile Ile Leu Gly Arg Tyr Phe Ala
237 385      390      395      400
239 Arg His Lys Gly Thr Tyr Phe Thr His Glu Ala Lys Gly Ala Asp Asp
240      405      410      415
242 Ala Ala Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu Gly Gly Gln Asn
243      420      425      430
245 Asn Ser Glu Glu Lys Lys Glu Tyr Phe Ile
246      435      440

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248 <210> SEQ ID NO: 3

249 <211> LENGTH: 1935

250 <212> TYPE: DNA

251 <213> ORGANISM: mus musculus

253 <220> FEATURE:

254 <221> NAME/KEY: CDS

255 <222> LOCATION: (2)..(1270)

256 <223> OTHER INFORMATION:

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260 Ala Ala Pro Pro Gly Leu Arg Leu Arg Leu Leu Leu Leu Leu Ser
261 1      5      10      15
263 gcc gcg gca ctg atc ccc aca ggt gat gga cag aat ctg ttt act aaa      97
264 Ala Ala Ala Leu Ile Pro Thr Gly Asp Gly Gln Asn Leu Phe Thr Lys
265      20      25      30
267 gac gtg aca gtg att gaa gga gaa gtg gca acc atc agc tgc cag gtc      145
268 Asp Val Thr Val Ile Glu Gly Glu Val Ala Thr Ile Ser Cys Gln Val
269      35      40      45
271 aat aag agt gac gac tca gtg atc cag ctc ctg aac ccc aac agg cag      193

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272	Asn	Lys	Ser	Asp	Asp	Ser	Val	Ile	Gln	Leu	Leu	Asn	Pro	Asn	Arg	Gln	
273		50					55					60					
275	acc	att	tac	ttc	agg	gac	ttc	agg	cct	ttg	aag	gac	agc	agg	ttt	cag	241
276	Thr	Ile	Tyr	Phe	Arg	Asp	Phe	Arg	Pro	Leu	Lys	Asp	Ser	Arg	Phe	Gln	
277	65					70					75				80		
279	ctg	ctg	aat	ttt	tct	agc	agt	gaa	ctc	aaa	gtg	tca	ctg	acg	aat	gtc	289
280	Leu	Leu	Asn	Phe	Ser	Ser	Ser	Glu	Leu	Lys	Val	Ser	Leu	Thr	Asn	Val	
281					85					90					95		
283	tca	atc	tcg	gat	gaa	ggg	aga	tac	ttc	tgc	cag	ctc	tac	acg	gac	ccc	337
284	Ser	Ile	Ser	Asp	Glu	Gly	Arg	Tyr	Phe	Cys	Gln	Leu	Tyr	Thr	Asp	Pro	
285				100					105					110			
287	cca	cag	gag	agt	tac	acc	acc	atc	aca	gtc	ctg	gtt	cct	cca	cgt	aac	385
288	Pro	Gln	Glu	Ser	Tyr	Thr	Thr	Ile	Thr	Val	Leu	Val	Pro	Pro	Arg	Asn	
289		115					120					125					
291	ttg	atg	atc	gat	atc	cag	aaa	gac	acg	gca	gtt	gaa	ggg	gag	gag	att	433
292	Leu	Met	Ile	Asp	Ile	Gln	Lys	Asp	Thr	Ala	Val	Glu	Gly	Glu	Glu	Ile	
293		130				135					140						
295	gaa	gtc	aac	tgt	act	gcc	atg	gcc	agc	aag	cca	gcg	acg	acc	atc	agg	481
296	Glu	Val	Asn	Cys	Thr	Ala	Met	Ala	Ser	Lys	Pro	Ala	Thr	Thr	Ile	Arg	
297	145				150					155					160		
299	tgg	ttc	aaa	ggg	aac	aag	gaa	ctc	aaa	ggc	aaa	tca	gag	gtg	gag	gag	529
300	Trp	Phe	Lys	Gly	Asn	Lys	Glu	Leu	Lys	Gly	Lys	Ser	Glu	Val	Glu	Glu	
301				165					170						175		
303	tgg	tcg	gac	atg	tac	act	gtg	acc	agt	cag	ctg	atg	ctg	aag	gtg	cac	577
304	Trp	Ser	Asp	Met	Tyr	Thr	Val	Thr	Ser	Gln	Leu	Met	Leu	Lys	Val	His	
305				180					185					190			
307	aag	gag	gac	gac	ggg	gtc	ccg	gtg	atc	tgc	cag	gtg	gag	cac	cct	gcg	625
308	Lys	Glu	Asp	Asp	Gly	Val	Pro	Val	Ile	Cys	Gln	Val	Glu	His	Pro	Ala	
309			195				200						205				
311	gtc	act	gga	aac	ctg	cag	acc	cag	cgc	tat	cta	gaa	gtg	cag	tat	aaa	673
312	Val	Thr	Gly	Asn	Leu	Gln	Thr	Gln	Arg	Tyr	Leu	Glu	Val	Gln	Tyr	Lys	
313		210				215					220						
315	ccg	caa	gtg	cat	atc	cag	atg	act	tac	cct	ctg	caa	ggc	cta	acc	cgg	721
316	Pro	Gln	Val	His	Ile	Gln	Met	Thr	Tyr	Pro	Leu	Gln	Gly	Leu	Thr	Arg	
317	225				230					235					240		
319	gaa	ggg	gat	gca	ttt	gag	tta	acg	tgt	gaa	gcc	atc	ggg	aag	ccc	cag	769
320	Glu	Gly	Asp	Ala	Phe	Glu	Leu	Thr	Cys	Glu	Ala	Ile	Gly	Lys	Pro	Gln	
321				245					250					255			
323	cct	gtg	atg	gta	act	tgg	gtg	aga	gtc	gat	gat	gaa	atg	cct	caa	cat	817
324	Pro	Val	Met	Val	Thr	Trp	Val	Arg	Val	Asp	Asp	Glu	Met	Pro	Gln	His	
325				260					265					270			
327	gcc	gta	ctg	tct	ggg	cca	aac	ctg	ttc	atc	aat	aac	cta	aac	aaa	aca	865
328	Ala	Val	Leu	Ser	Gly	Pro	Asn	Leu	Phe	Ile	Asn	Asn	Leu	Asn	Lys	Thr	
329			275				280						285				
331	gat	aac	ggt	act	tac	cgc	tgt	gag	gct	tcc	aac	ata	gtg	gga	aag	gct	913
332	Asp	Asn	Gly	Thr	Tyr	Arg	Cys	Glu	Ala	Ser	Asn	Ile	Val	Gly	Lys	Ala	
333		290				295					300						
335	cat	tcg	gac	tat	atg	ctg	tat	gta	tac	gat	ccc	ccc	aca	act	atc	cct	961
336	His	Ser	Asp	Tyr	Met	Leu	Tyr	Val	Tyr	Asp	Pro	Pro	Thr	Thr	Ile	Pro	

VERIFICATION SUMMARY

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